RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/562,942_

Source: _1 FWP_

Date Processed by STIC: _1/10/06_

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/562,942   TIME: 08:53:10

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J562942.raw

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     3 <110> APPLICANT: DOI, Hirofumi
     4        SAITO, Ken
     6 <120> TITLE OF INVENTION: Inhibition of Nerve Cell Death by Inhibiting Degradation of
SHC3, ATF6 or
     7        CREBL1 by HtrA2 and Method of Ameliorating Neurodegenerative Diseases
     9 <130> FILE REFERENCE: 3190-088
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/562,942
    12 <141> CURRENT FILING DATE: 2005-12-29
    14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/014378
    15 <151> PRIOR FILING DATE: 2004-09-30
    17 <150> PRIOR APPLICATION NUMBER: JP P2003-342588
    18 <151> PRIOR FILING DATE: 2003-09-30
    20 <160> NUMBER OF SEQ ID NOS: 37
    22 <170> SOFTWARE: PatentIn version 3.1
    24 <210> SEQ ID NO: 1
    25 <211> LENGTH: 1377
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Homo sapiens
    29 <220> FEATURE:
    30 <221> NAME/KEY: misc_feature
    31 <223> OTHER INFORMATION: DNA that codes for HtrA2 precursor protein
    34 <400> SEQUENCE: 1
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    37 gggggcattc gctgggggag gagaccccgt ttgaccccctg acctccgggc cctgctgacg     120
    39 tcaggaactt ctgacccccg ggcccgagtg acttatggga cccccagtct ctgggcccgg     180
    41 ttgtctgttg gggtcactga accccgagca tgcctgacgt ctgggacccc gggtccccgg     240
    43 gcacaactga ctgcggtgac cccagatacc aggacccggg aggcctcaga gaactctgga     300
    45 acccgttcgc gcgcgtggct ggcggtggcg ctgggcgctg ggggggcagt gctgttgttg     360
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    49 gcttctcccc ggagtcagta caacttcatc gcagatgtgg tggagaagac agcacctgcc     480
    51 gtggtctata tcgagatcct ggaccggcac cctttcttgg gccgcgaggt ccctatctcg     540
    53 aacggctcag gattcgtggt ggctgccgat gggctcattg tcaccaacgc ccatgtggtg     600
    55 gctgatcggc gcagagtccg tgtgagactg ctaagcggcg cacgtatga ggccgtggtc      660
    57 acagctgtgg atcccgtggc agacatcgca acgctgagga ttcagactaa ggagcctctc     720
    59 cccacgctgc ctctgggacg ctcagctgat gtccggcaag gggagtttgt tgttgccatg     780
    61 ggaagtccct ttgcactgca gaacacgatc acatccggca ttgttagctc tgctcagcgt     840
    63 ccagccagag acctgggact ccccccaaacc aatgtggaat acattcaaac tgatgcagct     900
    65 attgattttg gaaactctgg aggtcccctg gttaacctgg atggggaggt gattggagtg     960
    67 aacaccatga aggtcacagc tggaatctcc tttgccatcc cttctgatcg tcttcgagag    1020
    69 tttctgcatc gtgggggaaaa gaagaattcc tcctccggaa tcagtgggtc ccagcggcgc    1080
    71 tacattgggg tgatgatgct gaccctgagt cccagcatcc ttgctgaact acagcttcga    1140
    73 gaaccaagct ttcccgatgt tcagcatggt gtactcatcc ataaagtcat cctgggctcc    1200
    75 cctgcacacc gggctggtct gcggcctggt gatgtgattt tggccattgg ggagcagatg    1260
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84  <212> TYPE: PRT
85  <213> ORGANISM: Homo sapiens
87  <220> FEATURE:
88  <221> NAME/KEY: misc_feature
89  <223> OTHER INFORMATION: HtrA2 precursor protein
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98  Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
99              20                  25                  30
102 Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
103         35                  40                  45
106 Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly
107     50                  55                  60
110 Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
111 65                  70                  75                  80
114 Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
115                 85                  90                  95
118 Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
119             100                 105                 110
122 Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro
123         115                 120                 125
127 Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Ala Ser Pro Arg
128     130                 135                 140
131 Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
132 145                 150                 155                 160
135 Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
136             165                 170                 175
139 Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu
140             180                 185                 190
143 Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val
144         195                 200                 205
147 Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
148     210                 215                 220
151 Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu
152 225                 230                 235                 240
155 Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe
156             245                 250                 255
159 Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser
160         260                 265                 270
163 Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro
164         275                 280                 285
167 Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly
168     290                 295                 300
171 Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val
172 305                 310                 315                 320
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RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/562,942   TIME: 08:53:10

Input Set : A:\PTO.DA.txt
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175 Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp
176             325                 330                 335
179 Arg Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser
180             340                 345                 350
183 Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr
184         355                 360                 365
187 Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe
188     370                 375                 380
191 Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser
192 385                 390                 395                 400
195 Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile
196             405                 410                 415
199 Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg
200             420                 425                 430
203 Thr Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu
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208     450                 455
211 <210> SEQ ID NO: 3
212 <211> LENGTH: 981
213 <212> TYPE: DNA
214 <213> ORGANISM: Homo sapiens
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <223> OTHER INFORMATION: DNA that codes for mature HtrA2
221 <400> SEQUENCE: 3
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224 gtggtggaga agacagcacc tgccgtggtc tatatcgaga tcctggaccg gcaccctttc     120
226 ttgggccgcg aggtccctat ctcgaacggc tcaggattcg tggtggctgc cgatgggctc     180
228 attgtcacca acgcccatgt ggtggctgat cggcgcagag tccgtgtgag actgctaagc     240
230 ggcgacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcaacgctg     300
232 aggattcaga ctaaggagcc tctccccacg ctgcctctgg gacgctcagc tgatgtccgg     360
234 caaggggagt tgttgttgc catgggaagt ccctttgcac tgcagaacac gatcacatcc     420
236 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactccccca aaccaatgtg     480
238 gaatacattc aaactgatgc agctattgat tttggaaact ctggaggtcc cctggttaac     540
240 ctggatgggg aggtgattgg agtgaacacc atgaaggtca gctggaat ctcctttgcc      600
242 atcccttctg atcgtcttcg agagtttctg catcgtgggg aaaagaagaa ttcctcctcc     660
244 ggaatcagtg ggtcccagcg cgcgctacat ggggtgatga tgctgaccct gagtcccagc     720
246 atccttgctg aactacagct tcgagaacca agctttcccg atgttcagca tggtgtactc     780
248 atccataaag tcatcctggg ctcccctgca caccgggctg gtctgcggcc tggtgatgtg     840
250 attttggcca ttggggagca gatggtacaa aatgctgaag atgtttatga agctgttcga     900
252 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgtg     960
254 acccctgagg tcacagaatg a                                              981
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258 <211> LENGTH: 326
259 <212> TYPE: PRT
260 <213> ORGANISM: Homo sapiens
262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature
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264 <223> OTHER INFORMATION: mature HtrA2
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273 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
274             20                  25                  30
277 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
278         35                  40                  45
281 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
282     50                  55                  60
285 Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser
286 65                  70                  75                  80
289 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
290                 85                  90                  95
293 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
294             100                 105                 110
297 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met
298         115                 120                 125
301 Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser Gly Ile Val Ser
302     130                 135                 140
305 Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro Gln Thr Asn Val
306 145                 150                 155                 160
309 Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly Asn Ser Gly Gly
310                 165                 170                 175
313 Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val Asn Thr Met Lys
314             180                 185                 190
317 Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp Arg Leu Arg Glu
318         195                 200                 205
321 Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser Gly Ile Ser Gly
322     210                 215                 220
325 Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr Leu Ser Pro Ser
326 225                 230                 235                 240
329 Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe Pro Asp Val Gln
330             245                 250                 255
333 His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser Pro Ala His Arg
334             260                 265                 270
337 Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile Gly Glu Gln Met
338         275                 280                 285
341 Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg Thr Gln Ser Gln
342     290                 295                 300
345 Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu Thr Leu Tyr Val
346 305                 310                 315                 320
349 Thr Pro Glu Val Thr Glu
350                 325
353 <210> SEQ ID NO: 5
354 <211> LENGTH: 981
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial
358 <220> FEATURE:
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  359 <223> OTHER INFORMATION: Polynucleotide consisting of the same base sequence of SEQ
ID NO:
  360        3 wherein the nucleotide of position 520 is g
  362 <220> FEATURE:
  363 <221> NAME/KEY: misc_feature
  364 <223> OTHER INFORMATION: DNA that codes for mature HtrA2(S306A)
  367 <400> SEQUENCE: 5
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  370 gtggtggaga agacagcacc tgccgtggtc tatatcgaga tcctggaccg gcaccctttc     120
  372 ttgggccgcg aggtccctat ctcgaacggc tcaggattcg tggtggctgc cgatgggctc     180
  374 attgtcacca acgcccatgt ggtggctgat cggcgcagag tccgtgtgag actgctaagc     240
  376 ggcgacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcaacgctg     300
  378 aggattcaga ctaaggagcc tctccccacg ctgcctctgg gacgctcagc tgatgtccgg     360
  380 caaggggagt tgttgttgc catgggaagt ccctttgcac tgcagaacac gatcacatcc     420
  382 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactcccca aaccaatgtg     480
  384 gaatacattc aaactgatgc agctattgat tttggaaacg ctggaggtcc cctggttaac     540
  386 ctggatgggg aggtgattgg agtgaacacc atgaaggtca cagctggaat ctcctttgcc     600
  388 atcccttctg atcgtcttcg agagtttctg catcgtgggg aaaagaagaa ttcctcctcc     660
  390 ggaatcagtg ggtcccagcg cgcgctacat ggggtgatga tgctgaccct gagtcccagc     720
  392 atccttgctg aactacagct tcgagaacca agctttcccg atgttcagca tggtgtactc     780
  394 atccataaag tcatcctggg ctcccctgca caccgggctg gtctgcggcc tggtgatgtg     840
  396 attttggcca ttggggagca gatggtacaa aatgctgaag atgtttatga agctgttcga     900
  398 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgtg     960
  400 accctgagg tcacagaatg a                                               981
  403 <210> SEQ ID NO: 6
  404 <211> LENGTH: 326
  405 <212> TYPE: PRT
  406 <213> ORGANISM: Artificial
  408 <220> FEATURE:
  409 <223> OTHER INFORMATION: Polypeptide consisting of the same amino acid sequence of
SEQ ID
  410        NO:4 wherein the 174th amino acid residue is substituted by Ala
  412 <220> FEATURE:
  413 <221> NAME/KEY: misc_feature
  414 <223> OTHER INFORMATION: mature HtrA2(S306A)
  417 <400> SEQUENCE: 6
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  420 1               5                   10                  15
  423 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
  424             20                  25                  30
  427 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
  428         35                  40                  45
  431 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
  432     50                  55                  60
  435 Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser
  436 65                  70                  75                  80
  439 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
  440             85                  90                  95
  443 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
  444             100                 105                 110
  447 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/10/2006
PATENT APPLICATION: **US/10/562,942**   TIME: 08:53:11

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J562942.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36
Seq#:37

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/562,942**

DATE: 01/10/2006
TIME: 08:53:11

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J562942.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number